

1/17

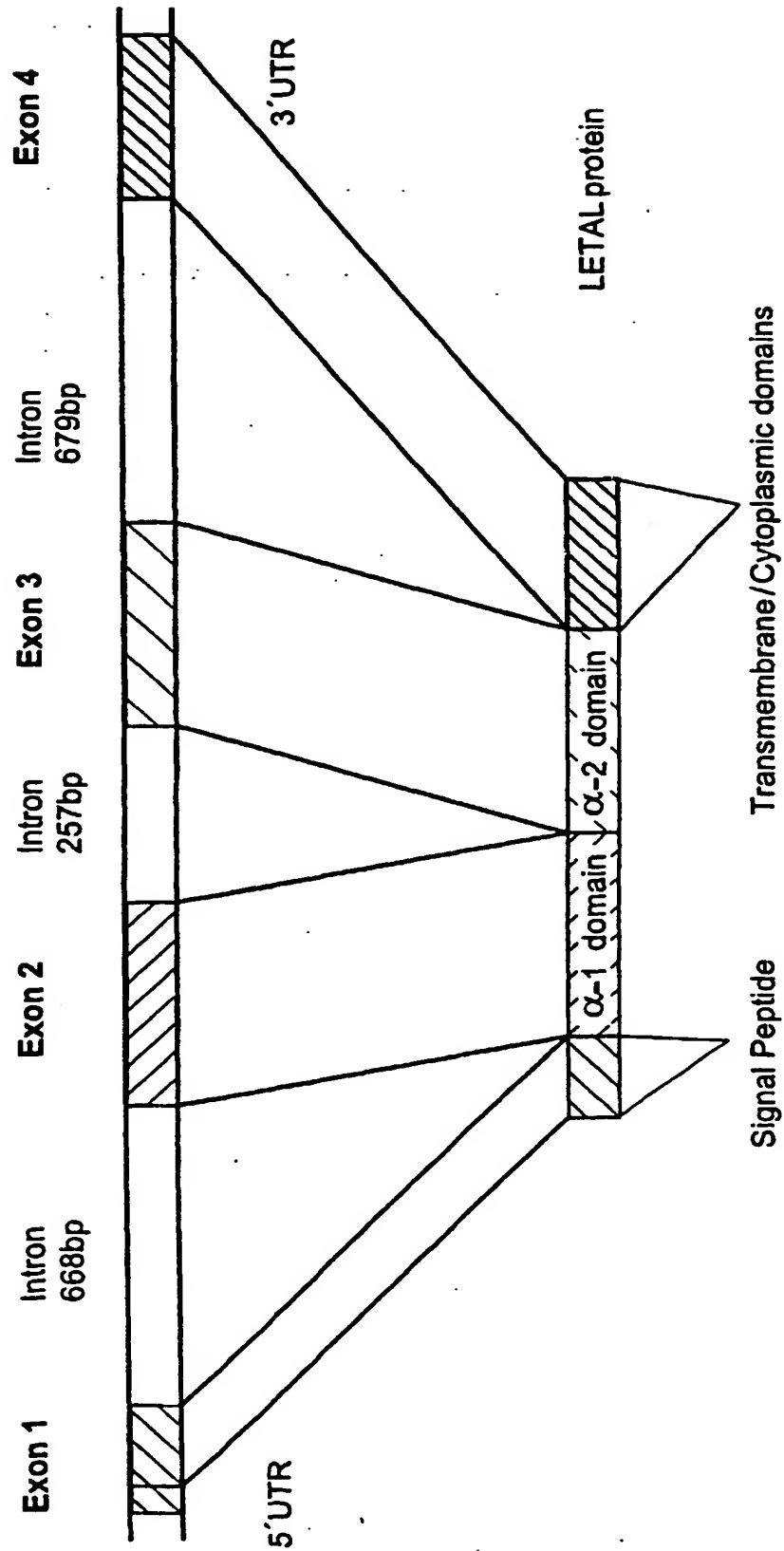


Fig. 1A

BEST AVAILABLE COPY

2/17

	-----Signal Peptide-----	
ULBP1	MAAAASPALLCLPLL-HLLSGWSRAGWV DTHCLCYDFFITTPKSRPEPQWCEVQGLVDER	
ULBP2	MAAAAATKILLCLPLL-LLLSGWSRAGRA DPHSLCYDITVTPKFRPGPRWCAVQGGQVDEK	
ULBP3	MAAAAAPAILPRLAIPYLLPFDWSGTGRA DAHSLWYNFTIIHLPRHGQQWCEVQSQVDQK	
Letal	-MRRISLTSSPVRLLFLLLLLIALEIMV GHSLSLCEFNFTIKSLSRPGQFWCEAQVFLNKN	
	----- α -1 domain-----	
ULBP1	PFLHYDCVNHKAKAFASLGKKVNVTKTMEEQTETLRDVVDFFLRGQLLDIQVENLIPIE PL	
ULBP2	TEFLHYDCGNKTVTPVSPFLGKKLVNVTAMKAQNPVLRREVVDIILTEQLRDIQLENYTPKE PL	
ULBP3	NFLSYDCGSDKVLSMGHLEEQLYATDAMGKQLEMLREVVGQRLRLLELADTELEDFTPSG PL	
Letal	LFLQYNSDNNMVKPLGLLGKKVYATSTWGETQTLEGEVGRDLRMLLCDIKPQIKTS-D PS	
	----- α -2 domain-----	
ULBP1	TLQARMSCHEAHGHGRGSWQFLFNGQKFFLFEDSNNRKWTALHPGAKKMTKWKENRDVT	
ULBP2	TLQARMSCHEQKAEHGHSSGSWQFSFDGQIFLFLFEDSEKRMWTTVHPGARMKKEKWKENDKVVA	
ULBP3	TLQVRMSCCEADGYIRGSWQFSFDGRKFFLFLFEDSNNRKWTVVHAGARRMKKEKWKDSGLT	
Letal	TLQVEVMFCQREAEKCTGASWQFATNGEKSLLFEDAMNMTWTVINHEASIKETWKKDRGLE	

ULBP1	MFFQKISLGDCKMWLEEFELMYWEQMLDPT K-----PPSLAPGTTQPKAMATT LSPWSLII	
ULBP2	MSFHYFSMGDCIGWLEDFLMGMDSTLEPS AG--APLAMSSGTTQLRATATT LILCCLLII	
ULBP3	TFFKMSMRDCKSWLRDFLMHRKKRLEPT A----PPTMAPGLAQPKAIAATT LSPWSFLII	
Letal	KYFERKLSKGDCHWLRREFLGHWEAMPEPT VSPVNASDIHWSSSSSLPDRWII LGAFILVVL	*****

ULBP1	FLCFILAGR-----	
ULBP2	LPCFILPGI-----	
ULBP3	L-CFILPGI-----	
Letal	MGIVLICVWW QNGEWQAGLWPLRTS	*****

Fig. 1B

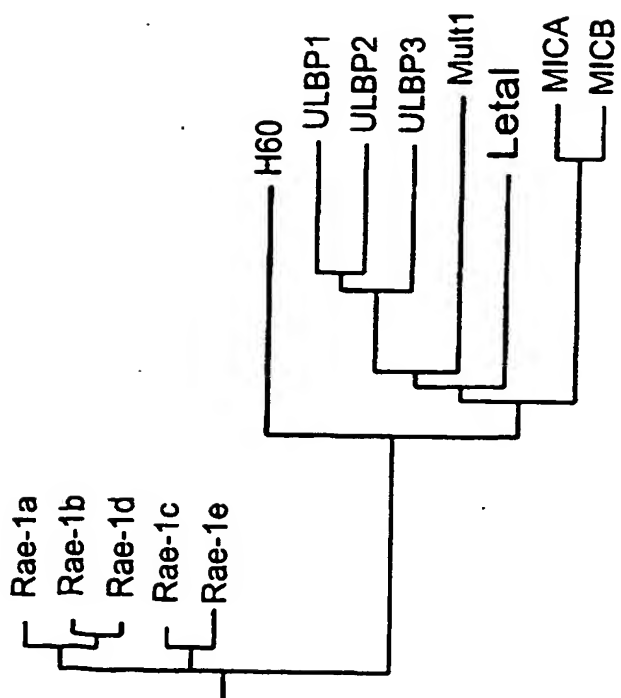
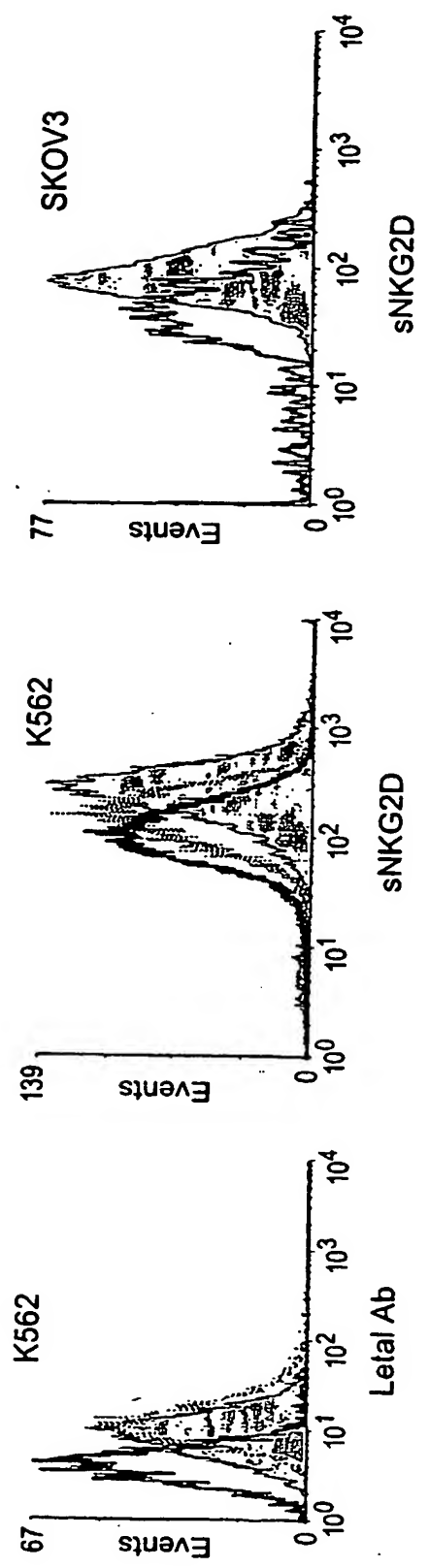


Fig. 1C

Fig. 1D



4/17

Exon 1

ACCATACAGTGAGGGTGAATGTGTACACGCCCCAGCTTCCTGCCTGTTACTCTCCACAGTATGCCAAGAATATCCCTGACT
TCTAGCCCTGTGCGCCTTCTTTTGTCTGCTGTTGCTACTAATAGCCTTGGAGATCATGGTTGGTG

Exon2

GTCACCTCTCTTTGCTTCAACTTCACCTATAAAATCATTTGCCAGACCTGGACAGCCCTGGTGTGAAGCGCAGGTCTTCTTGA
ATAAAAATCTTTTCCTTCAGTACAACAGTGACAACAACATGGTCAAACTCTGGCCCTCCTGGGGAAGAAGGTATATGCCCA
CCAGCACCTTGGGGAGAATTGACCCAAACGCTGGGAGAAGTGGGGCGAGACCTCAGGATGCTCCTTTGTGACATCAAAACCCC
AGATAAAGACCAGT

Exon3

GATCCTTCCACTCTGCAAGTCGAGATGTTTGTCAACGTGAAGCAGAACGGTGCATCCTGGCAGTTCGCCACC
AATGGAGAGAAATCCCTCCTCTTTGACGCAATGAACATGACCTGGACAGTAATTAATCATGAAGCCAGTAAAGATCAAGGAG
ACATGGAAAGAAAGACAGAGGGCTGGAAAAGTATTTCAAGGAAGCTCTCAAAAGGGAGACTGCGATCACTGGCTCAGGGAATTC
TTAGGGCACTGGGAGGCAATGCCAGAACCGACA

Exon4

GTGTACCCAGTAAATGCTTCAGATATCCACTGGTCTTCTAGTCTACCAGATAGATGGATCATCCTGGGGGCATTCAATC
CTGTTAGTTTAAATGGGAATTGTTCTCATCTGTCTGTGTCGCAAAATGGTGAGTGGCAGGCTGCTCTGGCCCTTGAGG
ACGTCTTAGTCTGGTAAG GACTCAAGAGAGGTTGAATCATGGG

Fig. 1E

5/17

1 - ACCATACAGTGAGGGTGAATGTGTACACGCCAGCTTCCTGCCTGTACTCTCCACAGT - 60
 61 - ATGCGAAGAAATATCCCTGACTTCTAGCCCTGTGCGCCTTCTTTTGTCTGCTGTGCTA - 120
 - M R I S L T S S P V R L L L F L L L L
 121 - CTAATAGCCTTGGAGATCATGGTTGGTGGTCACTCTCTTTGCTTCAACTTCACTATAAAA - 180
 - L I A L E I M V G G H S L C F N F T I K
 181 - TCATTGTCCAGACCTGGACAGCCCTGGTGTGAAGCGCAGGTCTTCTTGAATAAAAATCTT - 240
 - S L S R P G Q P W C E A Q V F L N K N L
 241 - TTCCTTCAGTACAACAGTGACAACAACATGGTCAAACCTCTGGGCCTCCTGGGGAAGAAG - 300
 - F L Q Y N S D N N M V K P L G L L G K K
 301 - GTATATGCCACCGCACTTGGGGAGAATTGACCCAAACGCTGGGAGAAGTGGGGCGAGAC - 360
 - V Y A T S T W G E L T Q T L G E V G R D
 361 - CTCAGGATGCTCCTTTGTGACATCAAACCCAGATAAAGACCAGTGATCCTTCCACTCTG - 420
 - L R M L L C D I K P Q I K T S D P S T L
 421 - CAAGTCGAGATGTTTGTCAACGTGAAGCAGAACGGTGCACCTGGTGCATCCTGGCAGTTC - 480
 - Q V E M F C Q Q R E A E R C T G A S W Q F
 481 - GCCACCAATGGAGAGAAATCCCTCCTTTGACGCAATGAACATGACCTGGACAGTAATT - 540
 - A T N G E K S L L F D A M N M T W T V I
 541 - AATCATGAAGCCAGTAAGATCAAGGAGACATGGAAGAAAGACAGAGGGCTGGAAAAGTAT - 600
 - N H E A S K I K E T W K K D R G L E K Y
 601 - TTCAGGAAGCTCTCAAAGGGAGACTGGATCACTGGCTCAGGGAATTTTAGGGCACTGG - 660
 - F R K L S K G D C D H W L R E F L G H W
 661 - GAGGCAATGCCAGAACCGACAGTGTCAACCAGTAATGCTTCAGATATCCACTGGTCTTCT - 720
 - E A M P E P T V S P V N A S D I H W S S
 721 - TCTAGTCTACCAGATAGATGGATCATCCTGGGGGCATTCATCCTGTAGTTTAAATGGGA - 780
 - S S L P D R W I I L G A F I L L V L M G
 781 - ATTGTTCTCATCTGTGTGGCAAAATGGTGGCAGGCTGGTCTCTGGCCCTTG - 840
 - I V L I C V W W Q N G E W Q A G L W P L
 841 - AGGACGTCTTAGTCTGGTAAGGACTCAAGAGAGGTGAATCATGGG - 885
 - R T S *

Fig. 1F

6/17

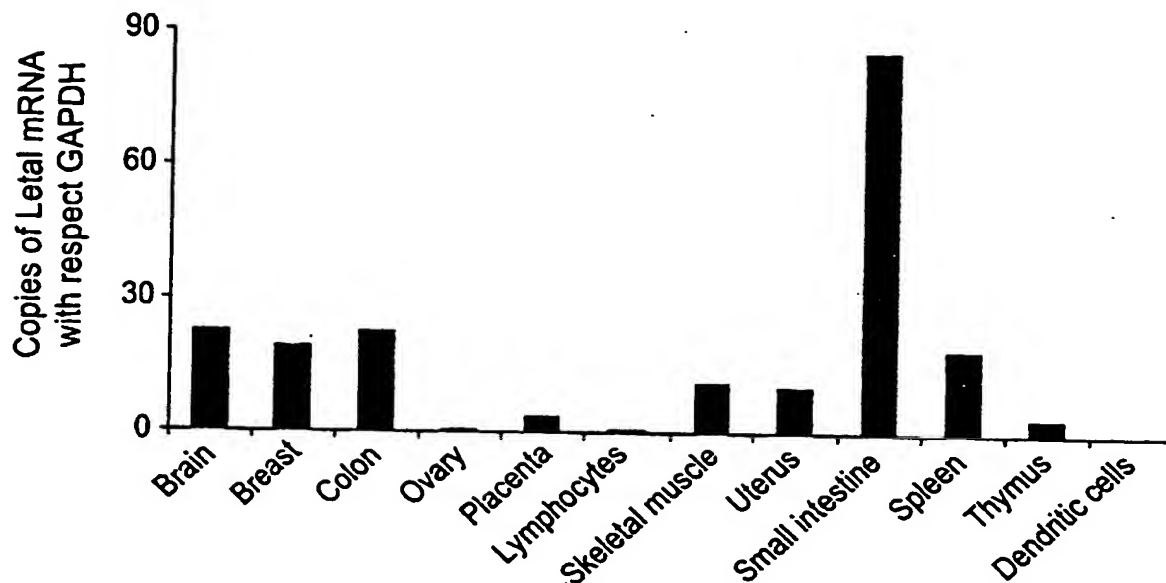


Fig. 2A

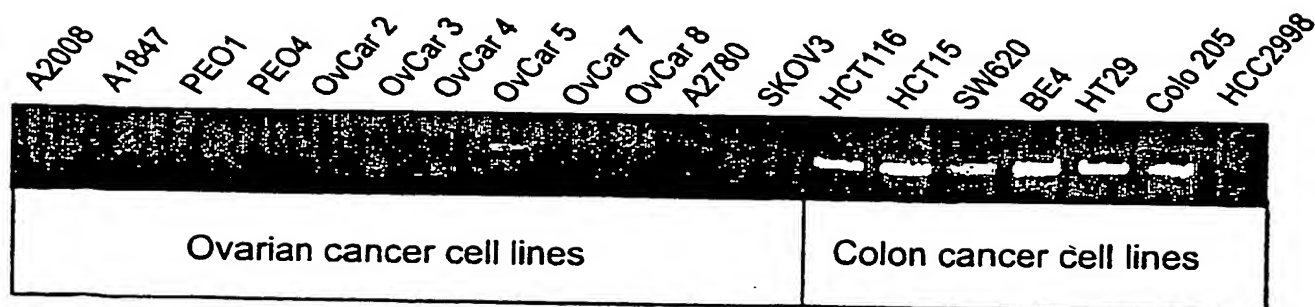


Fig. 2B

Fig. 3A

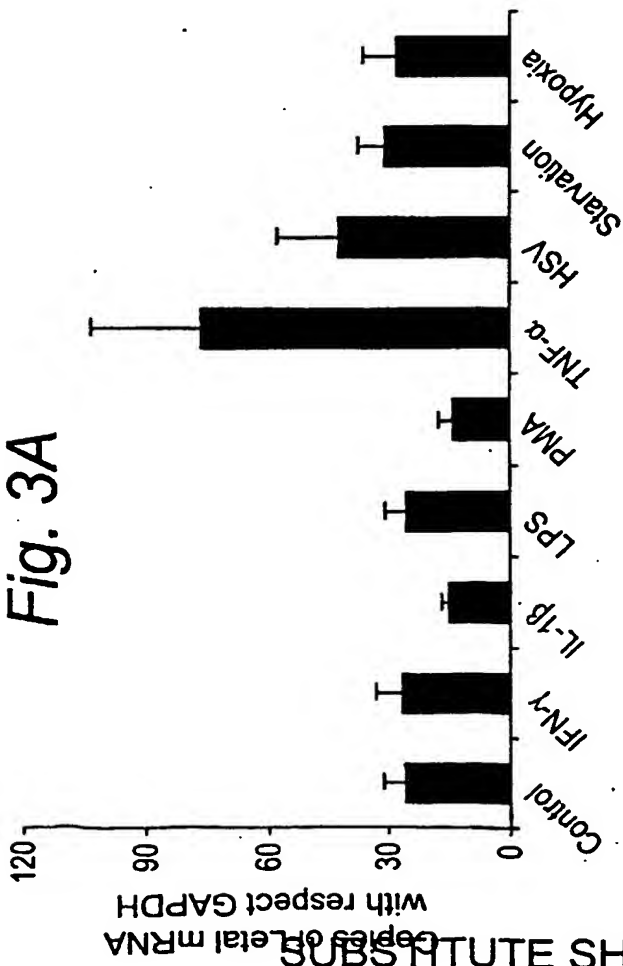
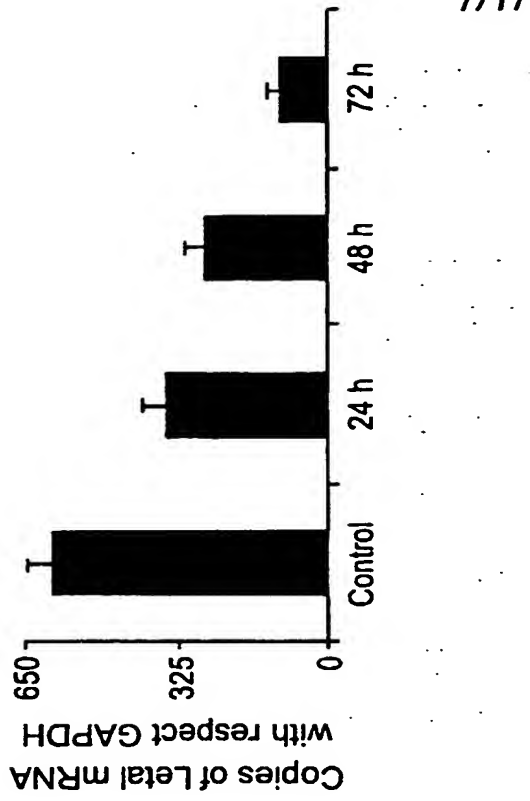


Fig. 3B



7/17

Fig. 3C

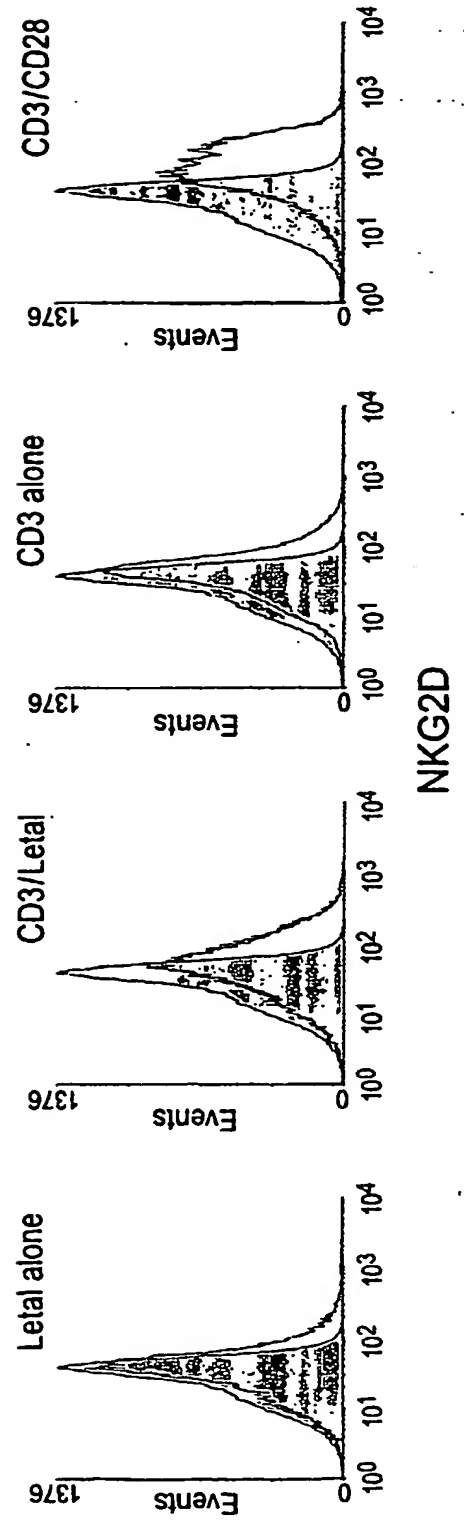


Fig. 4A

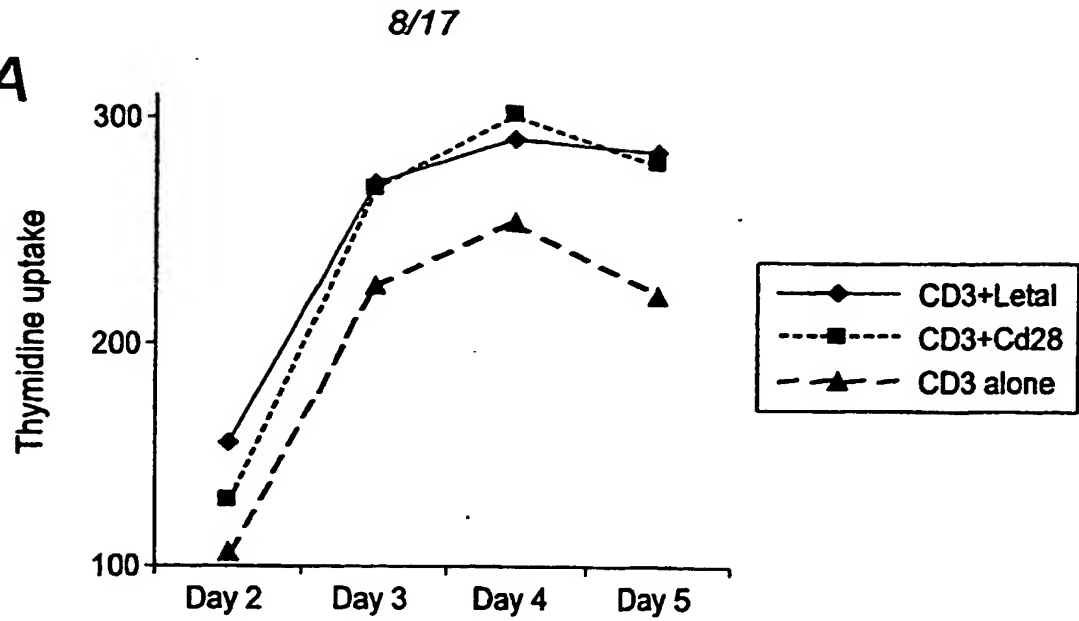


Fig. 4B

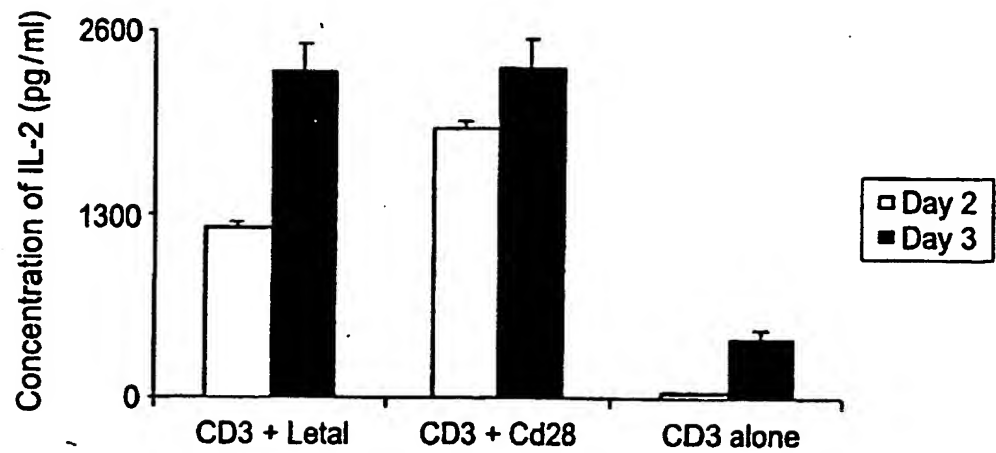
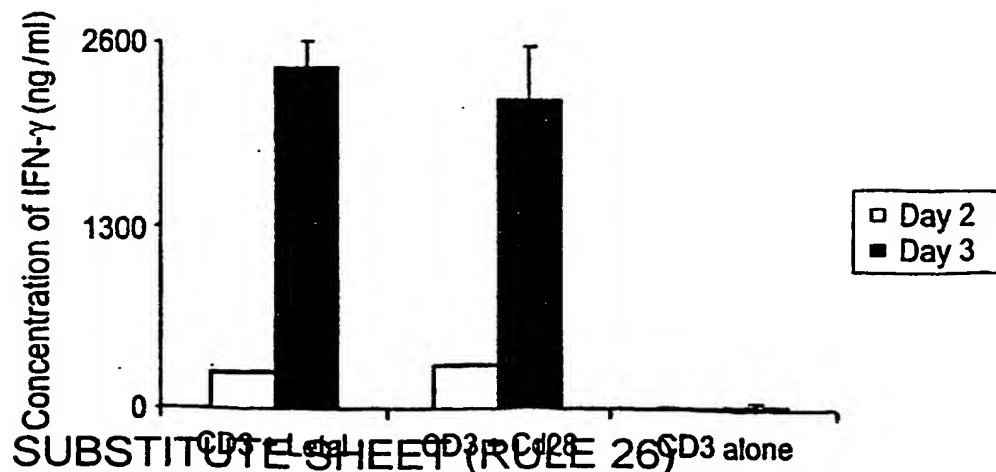


Fig. 4C



9/17

Fig. 5A

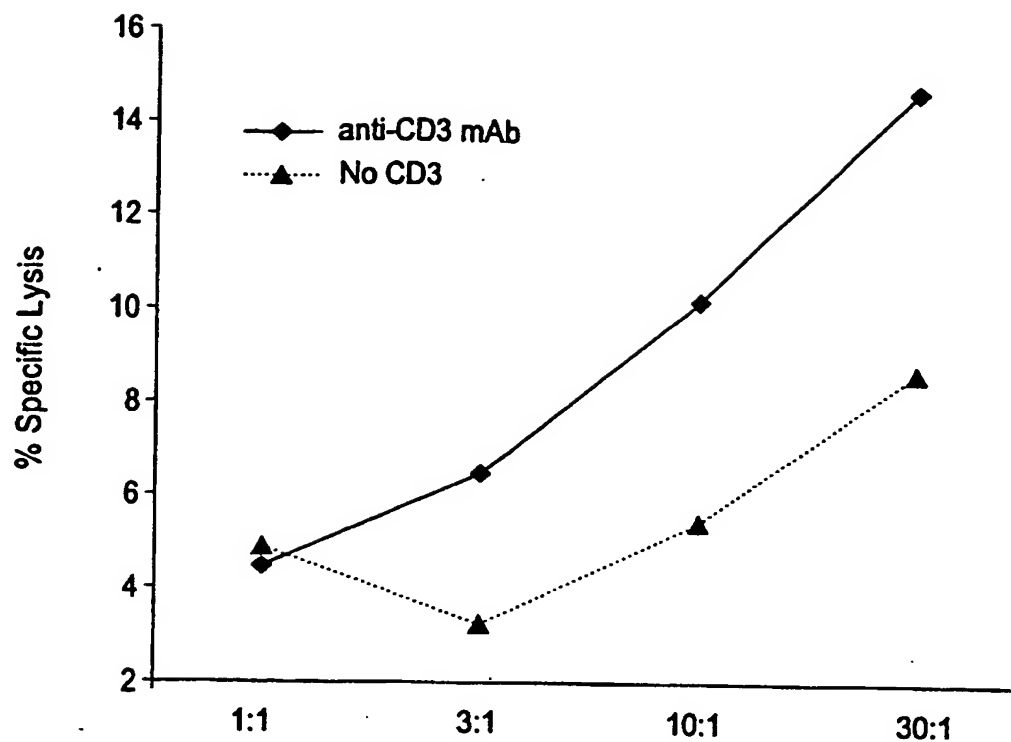
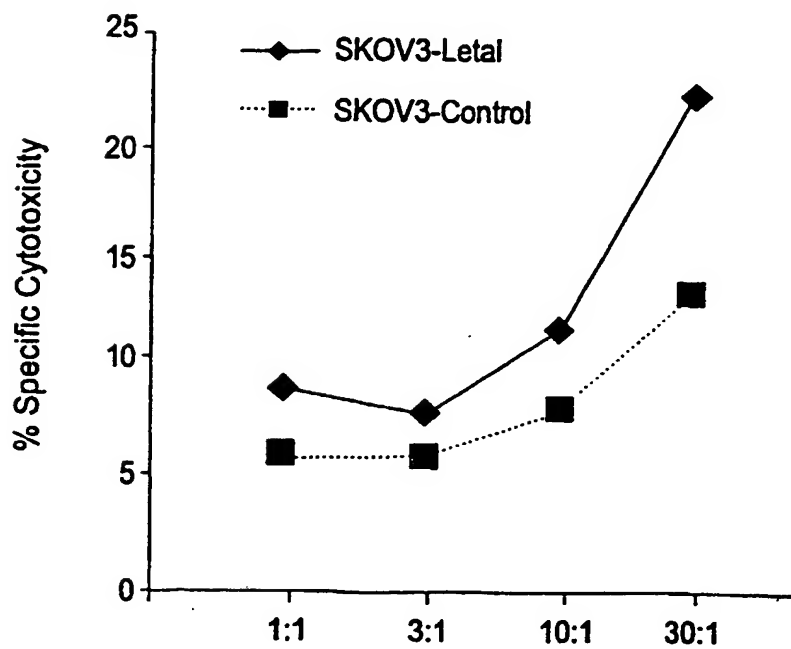
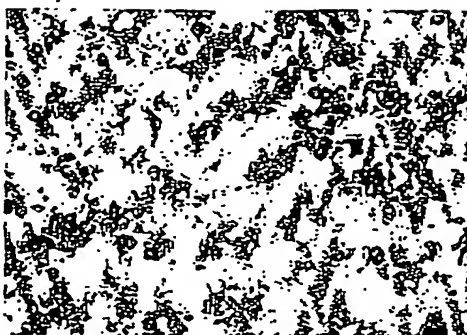
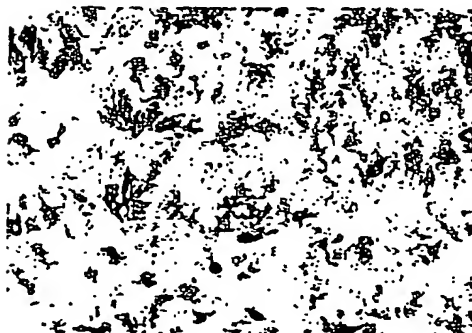
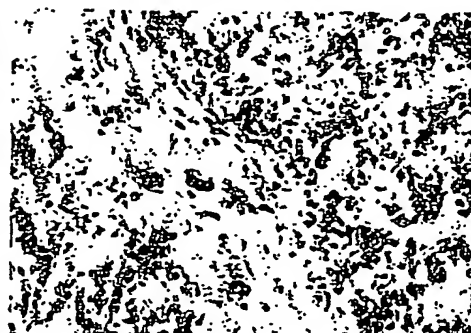
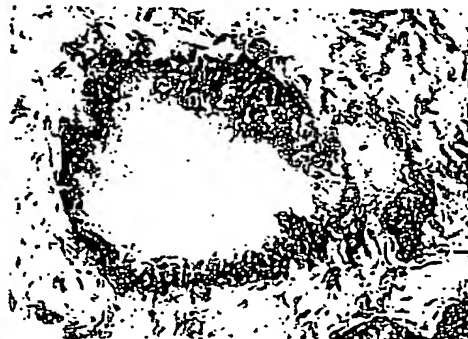


Fig. 5B



10/17

Fig. 6A*Fig. 6B**Fig. 6C**Fig. 6D**Fig. 6E**Fig. 6F*

11/17

Fig. 7A

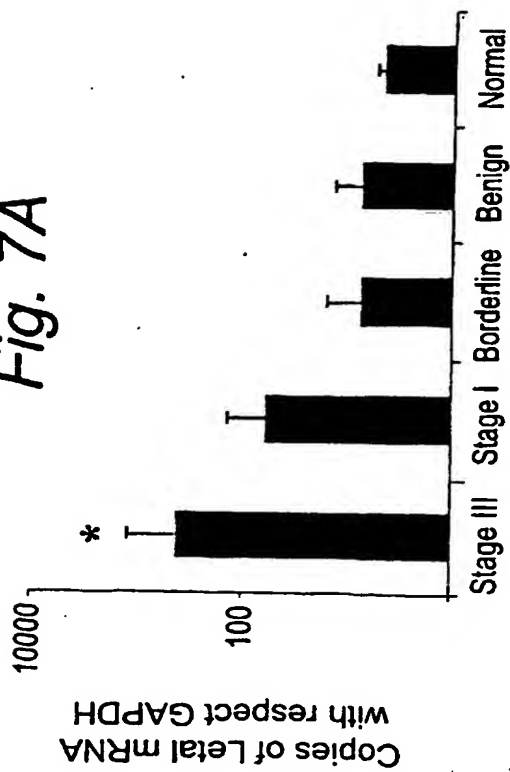


Fig. 7B

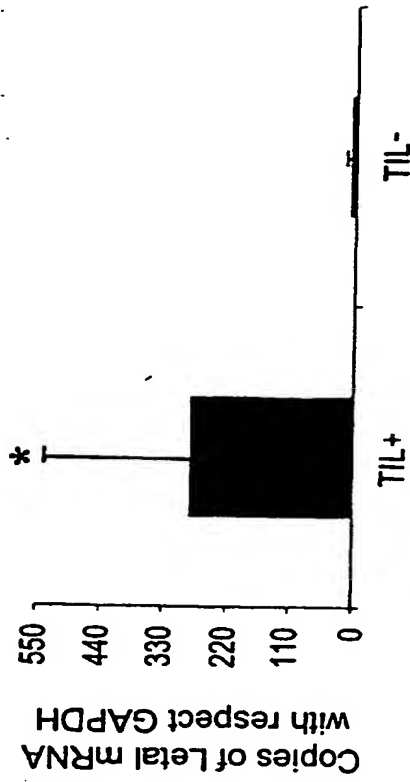


Fig. 7C

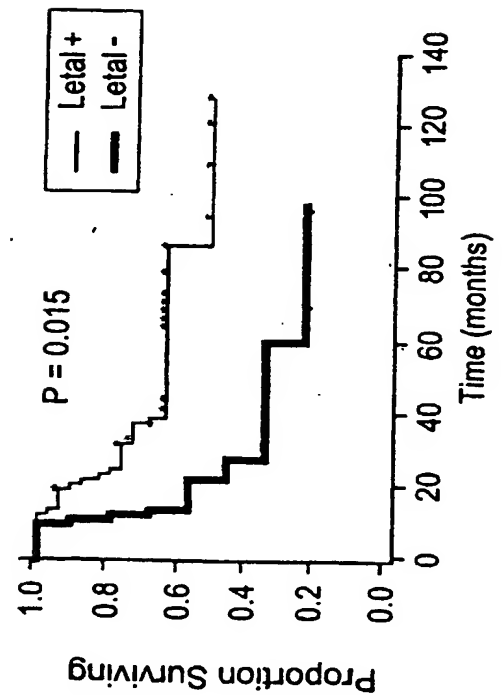
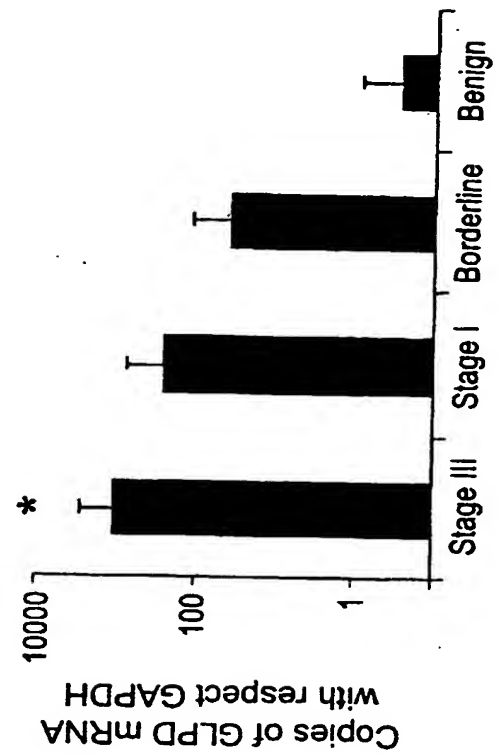


Fig. 7D



12/17

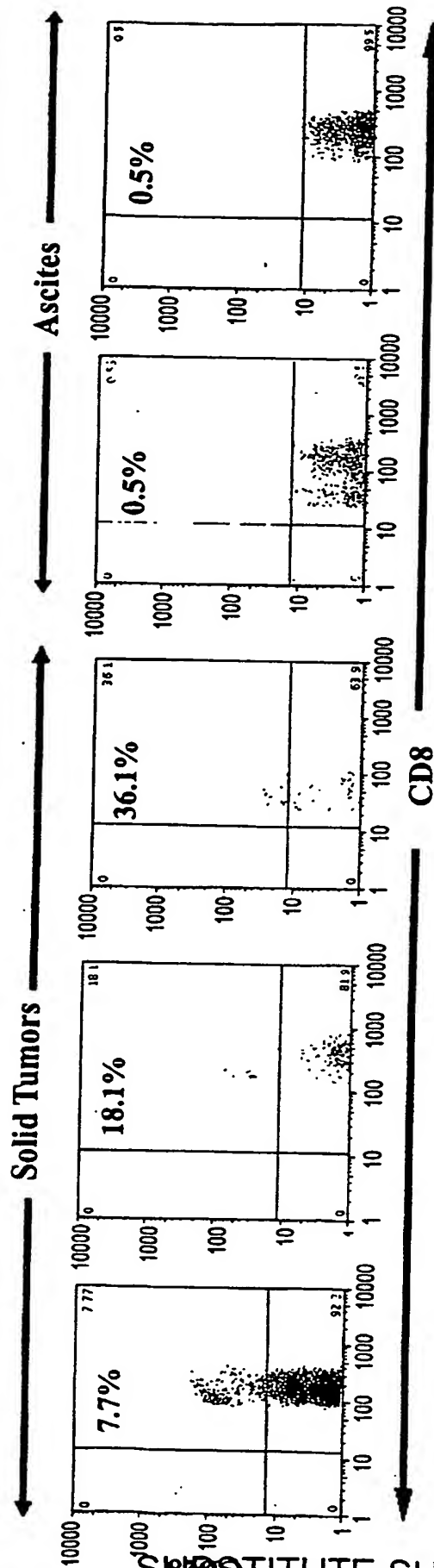


Fig. 8A

13/17

Fig. 8B

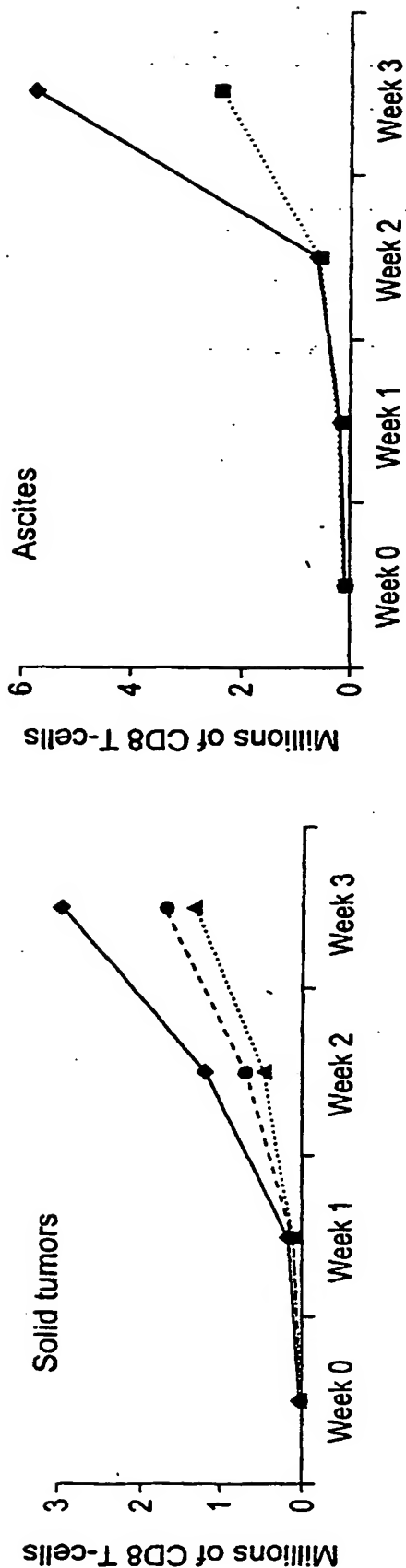
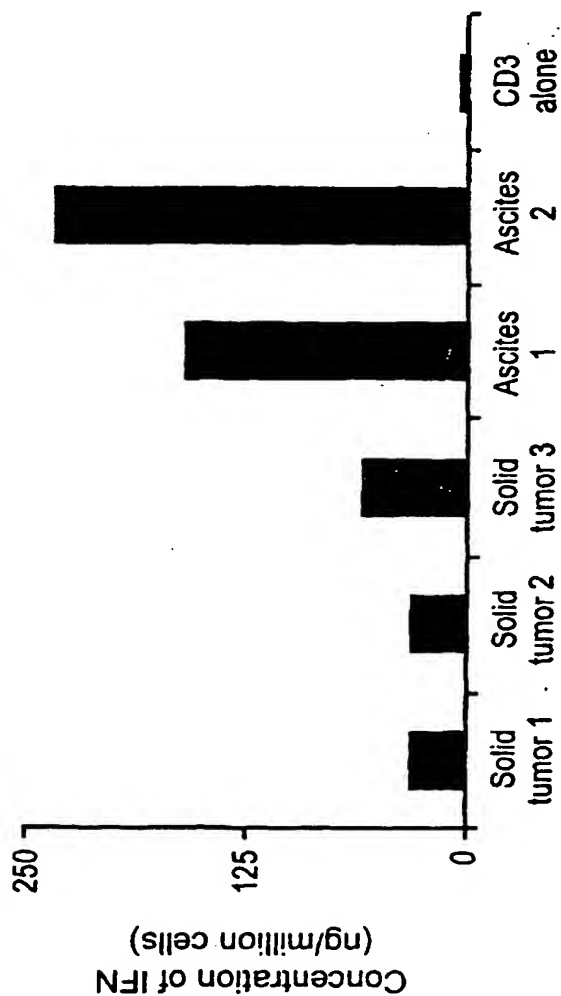


Fig. 8C



14/17

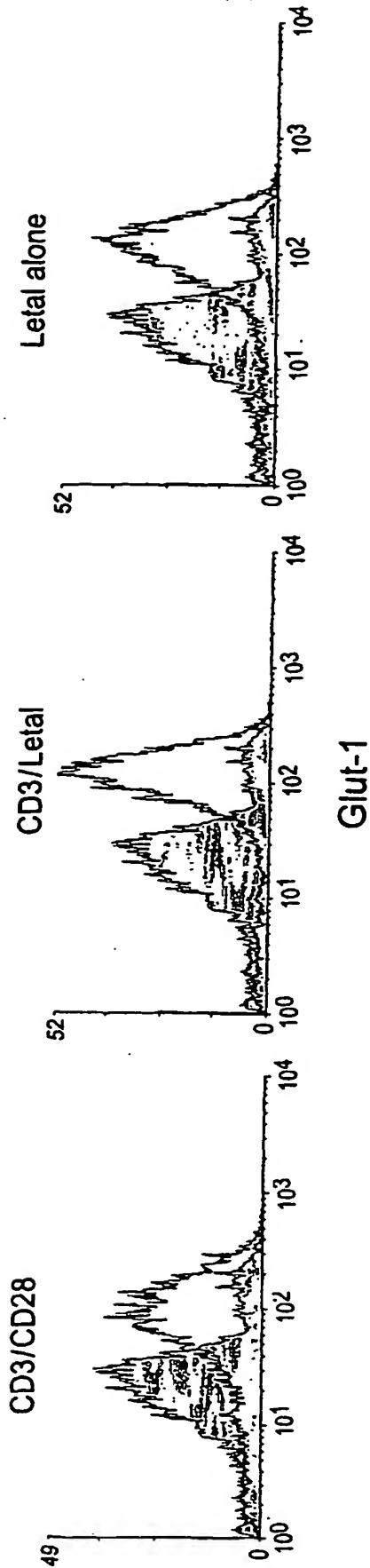


Fig. 9A

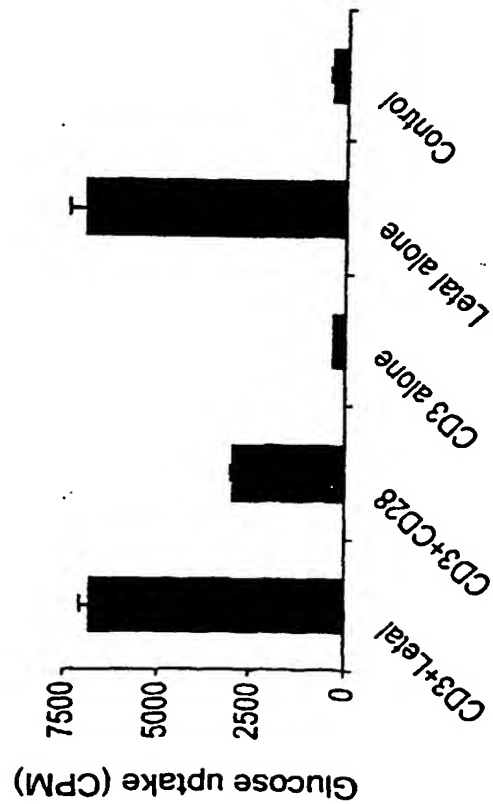


Fig. 9B

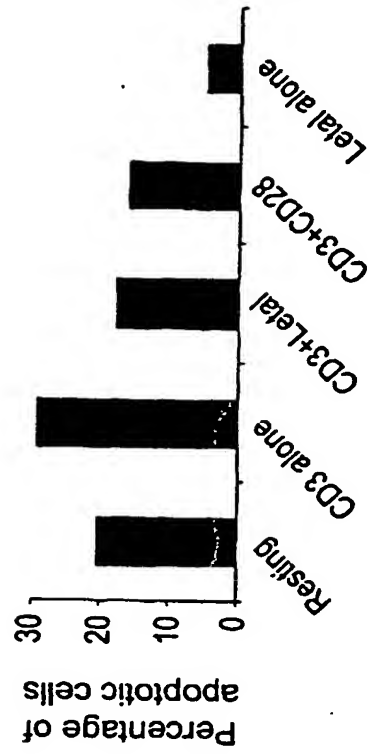


Fig. 9C

15/17



Fig. 10A

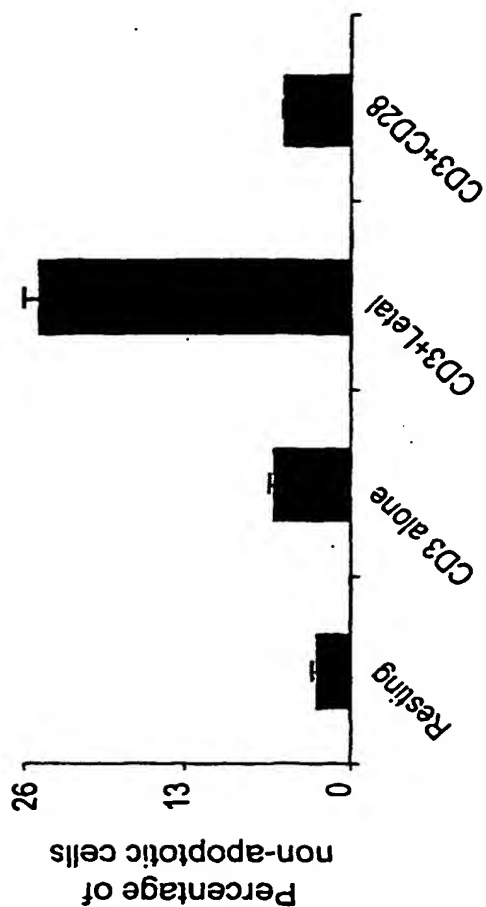
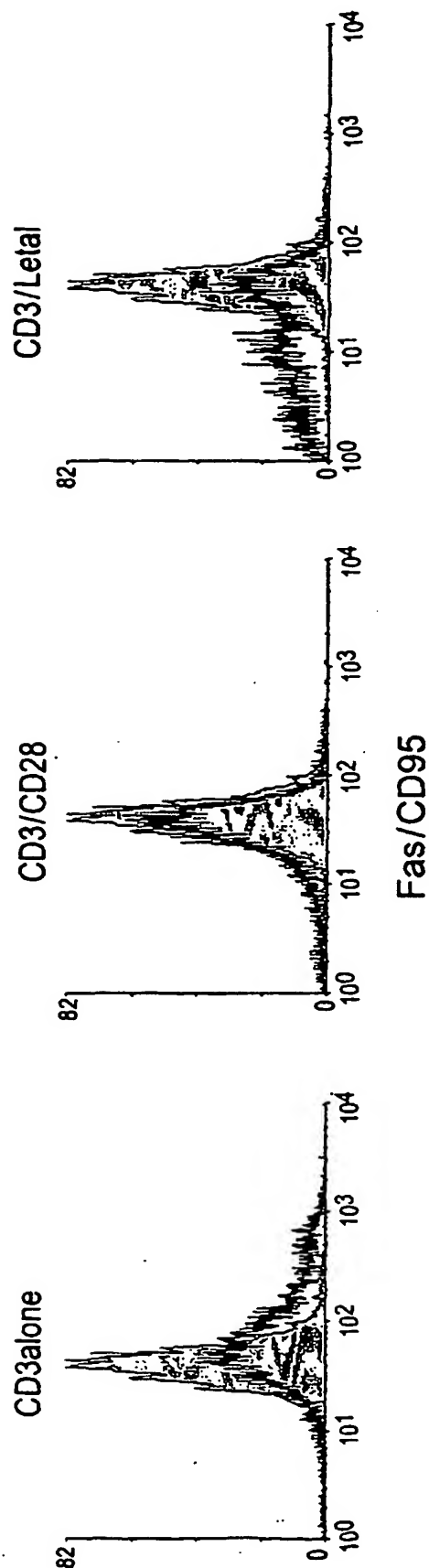


Fig. 10C

Fig. 10B



16/17

TTTCGAGCACATGTGTTTTTATGAGAATTATGCTGAGATAGATTCTTTACATATTCATCAATGTC
TGAAGAAGTTACTTATGCAGATCTTCAATCCAGAACTCCAGTGAGATGGAAAAAATCCAGAAAT
TGGCAAAATTGGGAAAAAGCACCTCCAGTCCCTCTCATGTATGGCGTCCAGCAGCCTTGTTTCT
GACTCTTCTGTGCCCTTCTGTGCTCATTTGGATTGGAGTCTTGGCAAGCATGTTTTCACGTAACCTT
GAAGATAGAAATGAAAAAATGAACAACTACAAACATCAGTGAAGAGCTCCAGAGAAATATTTT
TCTACAACTGATGAGTAACATGAATATCTCAACRAAGATCAGGAACCTCTCCACCACACTGCAAAC
AATAGCCACCAAATTATGTGCGTGAGCTATATAGCAAGAACAGAGACAAATGTAGCCTTGTC
AAGGAGATGGATTGGCATAAGGACAGCTGTTATTTCTTAAGTGATGATGTCCAAACATGGCAGGA
GAGTAAATGGCCTGTGCTGCTCAGAAATGCCAGCCTGTTGAAGATAAACAAACAAATGCATTGGA
ATTTATAAAATCCCAGAGTAGATCATATGACTATTGGCTGGGATTATCTCCTGAAGAAGATTCCAC
TCGTGTATGAGAGTGGATAATAATAATCAACTCCTCTGCCTGGTAAGTGT

Fig. 11

17/17

1 - TTCGAGCACATGTGTTTTTATGAGAATTATGCTGAGATAGATTCTTTACATATTCATCA - 60
- M C F Y E N Y A E I D F F T Y S S
61 - ATGTCTGAAGAAGTTACTTATGCAGATCTTCAATCCAGAACTCCAGTGAGATGGAAAAA - 120
- M S E E V T Y A D L Q F Q N S S E M E K
121 - ATCCCAGAAATTGGCAAATTTGGGAAAAAGCACCTCCAGCTCCCTCTCATGTATGGCGT - 180
- I P E I G K F G E K A P P A P S H V W R
181 - CCAGCAGCCTTGTTCTGACTCTTCTGTGCGCTTCTGTGCTCATTTGGAGTCTTG - 240
- P A A L F L T L L C L L L L L I G L G V L
241 - GCAAGCATGTTTCACGTAACCTTTGAAGATAGAAAATGAAAAAATGAACAACACTACAAAC - 300
- A S M F H V T L K I E M K K M N K L Q N
301 - ATCAGTGAAGAGCTCCAGAGAAATATTTCTTACAACTGATGAGTAACATGAATATCTCC - 360
- I S E E L Q R N I S L Q L M S N M N I S
361 - AACAAATCAGGAACCTCTCCACCACACTGCAAAACAATAGCCACCAATATGTCGTGAG - 420
- N K I R N L S T T L Q T I A T K L C R E
421 - CTATATAGCAAGAACAAGAGCACAAATGTAAGCCTTGTCCAAGGAGATGGATTGGCAT - 480
- L Y S K E Q E H K C K P C P R R W I W H
481 - AAGGACAGCTGTTATTTCCCTAAGTATGATGTCCAAACATGGCAGGAGAGTAAAAATGGCC - 540
- K D S C Y F L S D D V Q T W Q E S K M A
541 - TGTGCTGCTCAGAAATGCCAGCCTGTTGAAGATAAACAACAATAATGCAATGGAATTATA - 600
- C A A Q N A S L L K I N N K N A L E F I
601 - AAATCCCAGAGTAGATCATATGACTATTGGCTGGGATTATCTCTGAAGAAGATTCACACT - 660
- K S Q S R S Y D Y W L G L S P E E D S T
661 - CGTGGTATGAGAGTGGATAATAATCAACTCCTCTGCTGCTGTAAGTGT - 709
- R G M R V D N I I N S S A W *

Fig. 12

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☒ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☒ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☒ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☒ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.